# Package 'NGScopyData'

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**Type** Package

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**Title** Subset of BAM files of human tumor and pooled normal sequencing data (Zhao et al. 2014) for the NGScopy package

**Description** Subset of BAM files of human lung tumor and pooled normal samples by targeted panel sequencing. [Zhao et al 2014. Targeted Sequencing in Non-Small Cell Lung Cancer (NSCLC) Using the University of North Carolina (UNC) Sequencing Assay Captures Most Previously Described Genetic Aberrations in NSCLC. In preparation.] Each sample is a 10 percent random subsample drawn from the original sequencing data. The pooled normal sample has been rescaled accroding to the total number of normal samples in the ``pool". Here provided is the subsampled data on chr6 (hg19).

**License** GPL (>=2)

**LazyData** yes

**URL** [http://www.bioconductor.org/packages/release/data/experiment/html/NGScopyData.html](http://www.bioconductor.org/packages/release/data/experiment/html/NGScopyData.html)

**biocViews** ExperimentData, CancerData, LungCancerData, SequencingData

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NGScopyData-package        *Subset of BAM files of human tumor and pooled normal sequencing data (Zhao et al. 2014) for the NGScopy package*

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### Description

Subset of BAM files of human tumor and pooled normal samples by targeted panel sequencing (Zhao et al. 2014). Each sample is a 10 percent random subsample drawn from the original sequencing data. The pooled normal sample has been rescaled accroding to the total number of normal samples in the "pool". Here provided is the subsampled data on chr6 (hg19).

### Usage

```
tps_90.chr6()
tps_27.chr6()
tps_N8.chr6()
```

### Author(s)

Xiaobei Zhao

### References

Zhao et al (2014), Targeted Sequencing in Non-Small Cell Lung Cancer (NSCLC) Using the University of North Carolina (UNC) Sequencing Assay Captures Most Previously Described Genetic Aberrations in NSCLC. *In preparation*

### See Also

NGScopy

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tps_27.chr6 *A subset of tumor sample (ID: 27) by targeted panel sequencing*

---

### Description

A subset of tumor sample (ID: 27) by targeted panel sequencing, a 10 percent random subsample drawn from chr6, hg19 (Zhao et al. 2014).

### Usage

```
tps_27.chr6()
```

### Value

character, the path of the (sorted) bam file and its index file

### Author(s)

Xiaobei Zhao

### See Also

[NGScopyData](#) NGScopy

### Examples

```
require(NGScopyData)
tps_27.chr6()
```

---

tps_90.chr6 *A subset of tumor sample (ID: 90) by targeted panel sequencing*

---

### Description

A subset of tumor sample (ID: 90) by targeted panel sequencing, a 10 percent random subsample drawn from chr6, hg19 (Zhao et al. 2014).

### Usage

```
tps_90.chr6()
```

### Value

character, the path of the (sorted) bam file and its index file

### Author(s)

Xiaobei Zhao

### See Also

[NGScopyData](#) NGScopy

### Examples

```
require(NGScopyData)
tps_90.chr6()
```

---

| tps_N8.chr6 | *A subset of pooled normal sample (ID: N8) by targeted panel sequencing* |
|---|---|

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### Description

A subset of pooled normal sample (ID: N8) by targeted panel sequencing, a 10 percent random subsample, rescaled by the total number of normal samples in the "pool", drawn from chr6, hg19 (Zhao et al. 2014).

### Usage

```
tps_N8.chr6()
```

### Value

character, the path of the (sorted) bam file and its index file

### Author(s)

Xiaobei Zhao

### See Also

[NGScopyData](#) NGScopy

### Examples

```
require(NGScopyData)
tps_N8.chr6()
```

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